

Appendix III: Alignment of instant SEQ ID NO: 16 and GenBank Accession No. XM_003059

BLASTN 2.2.22+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: SN273YXF114

Query= SID_16
Length=1609

Sequences producing significant alignments:	Score (Bits)	E Value
ref XM_003059.3 Homo sapiens peroxisome proliferative activa...	2972	0.0

ALIGNMENTS

>ref|XM_003059.3| Homo sapiens peroxisome proliferative activated receptor, gamma (PPARG), mRNA
Length=1609

Score = 2972 bits (1609), Expect = 0.0
Identities = 1609/1609 (100%), Gaps = 0/1609 (0%)
Strand=Plus/Plus

Query	1	TTCAAGTCTTTTTCTTTTAACGGATTGATCTTTTGCTAGATAGAGACAAAATATCAGTGT	60
Sbjct	1	TTCAAGTCTTTTTCTTTTAACGGATTGATCTTTTGCTAGATAGAGACAAAATATCAGTGT	60
Query	61	GAATTACAGCAAACCCCTATTCCATGCTGTTATGGGTGAAACTCTGGGAGATTCTCCTAT	120
Sbjct	61	GAATTACAGCAAACCCCTATTCCATGCTGTTATGGGTGAAACTCTGGGAGATTCTCCTAT	120
Query	121	TGACCCAGAAAGCGATTTCCTTCACTGATACTGTCTGCAAACATATCACAAGAAATGAC	180
Sbjct	121	TGACCCAGAAAGCGATTTCCTTCACTGATACTGTCTGCAAACATATCACAAGAAATGAC	180
Query	181	CATGGTTGACACAGAGATGCCATTCTGGCCACCAACTTTGGGATCAGCTCCGTGGATCT	240
Sbjct	181	CATGGTTGACACAGAGATGCCATTCTGGCCACCAACTTTGGGATCAGCTCCGTGGATCT	240
Query	241	CTCCGTAATGGAAGACCACTCCCACTCCTTTGATATCAAGCCCTTCACTACTGTTGACTT	300
Sbjct	241	CTCCGTAATGGAAGACCACTCCCACTCCTTTGATATCAAGCCCTTCACTACTGTTGACTT	300
Query	301	CTCCAGCATTTCTACTCCACATTACGAAGACATTCCATTACACAAGAACAGATCCAGTGGT	360
Sbjct	301	CTCCAGCATTTCTACTCCACATTACGAAGACATTCCATTACACAAGAACAGATCCAGTGGT	360
Query	361	TGCAGATTACAAGTATGACCTGAAACTTCAAGAGTACCAAAGTGCAATCAAAGTGGAGCC	420
Sbjct	361	TGCAGATTACAAGTATGACCTGAAACTTCAAGAGTACCAAAGTGCAATCAAAGTGGAGCC	420
Query	421	TGCATCTCCACCTTATTATTCTGAGAAGACTCAGCTCTACAATAAGCCTCATGAAGAGCC	480
Sbjct	421	TGCATCTCCACCTTATTATTCTGAGAAGACTCAGCTCTACAATAAGCCTCATGAAGAGCC	480
Query	481	TTCCAACCTCCCTCATGGCAATTGAATGTCGTGTCTGTGGAGATAAAGCTTCTGGATTTCA	540

Sbjct	481	 TTCCAACCTCCCTCATGGCAATTGAATGTCGTGTCTGTGGAGATAAAGCTTCTGGATTTC	540
Query	541	CTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTCTTCCGGAGAACAATCAGATTGAA	600
Sbjct	541	 CTATGGAGTTCATGCTTGTGAAGGATGCAAGGGTTTCTTCCGGAGAACAATCAGATTGAA	600
Query	601	GCTTATCTATGACAGATGTGATCTTAACTGTCGGATCCACAAAAAAGTAGAAATAAATG	660
Sbjct	601	 GCTTATCTATGACAGATGTGATCTTAACTGTCGGATCCACAAAAAAGTAGAAATAAATG	660
Query	661	TCAGTACTGTCGGTTTCAGAAATGCCTTGCAGTGGGGATGTCTCATAATGCCATCAGGTT	720
Sbjct	661	 TCAGTACTGTCGGTTTCAGAAATGCCTTGCAGTGGGGATGTCTCATAATGCCATCAGGTT	720
Query	721	TGGGCGGATGCCACAGGCCGAGAAGGAGAAGCTGTTGGCGGAGATCTCCAGTGATATCGA	780
Sbjct	721	 TGGGCGGATGCCACAGGCCGAGAAGGAGAAGCTGTTGGCGGAGATCTCCAGTGATATCGA	780
Query	781	CCAGCTGAATCCAGAGTCCGCTGACCTCCGGGCCCTGGCAAAACATTTGTATGACTCATA	840
Sbjct	781	 CCAGCTGAATCCAGAGTCCGCTGACCTCCGGGCCCTGGCAAAACATTTGTATGACTCATA	840
Query	841	CATAAAGTCCTTCCCGCTGACCAAAGCAAAGGCGAGGGCGATCTTGACAGGAAAGACAAC	900
Sbjct	841	 CATAAAGTCCTTCCCGCTGACCAAAGCAAAGGCGAGGGCGATCTTGACAGGAAAGACAAC	900
Query	901	AGACAAATCACCATTTCGTTATCTATGACATGAATTCCTTAATGATGGGAGAAGATAAAAT	960
Sbjct	901	 AGACAAATCACCATTTCGTTATCTATGACATGAATTCCTTAATGATGGGAGAAGATAAAAT	960
Query	961	CAAGTTCAAACACATCACCCCCCTGCAGGAGCAGAGCAAAGAGGTGGCCATCCGCATCTT	1020
Sbjct	961	 CAAGTTCAAACACATCACCCCCCTGCAGGAGCAGAGCAAAGAGGTGGCCATCCGCATCTT	1020
Query	1021	TCAGGGCTGCCAGTTTCGCTCCGTGGAGGCTGTGCAGGAGATCACAGAGTATGCCAAAAG	1080
Sbjct	1021	 TCAGGGCTGCCAGTTTCGCTCCGTGGAGGCTGTGCAGGAGATCACAGAGTATGCCAAAAG	1080
Query	1081	CATTCTGGTTTTGTAAATCTTGACTTGAACGACCAAGTAACTCTCCTCAAATATGGAGT	1140
Sbjct	1081	 CATTCTGGTTTTGTAAATCTTGACTTGAACGACCAAGTAACTCTCCTCAAATATGGAGT	1140
Query	1141	CCACGAGATCATTTACACAATGCTGGCCTCCTTGATGAATAAAGATGGGGTTCTCATATC	1200
Sbjct	1141	 CCACGAGATCATTTACACAATGCTGGCCTCCTTGATGAATAAAGATGGGGTTCTCATATC	1200
Query	1201	CGAGGGCCAAGGCTTCATGACAAGGGAGTTTCTAAAGAGCCTGCGAAAGCCTTTTGGTGA	1260
Sbjct	1201	 CGAGGGCCAAGGCTTCATGACAAGGGAGTTTCTAAAGAGCCTGCGAAAGCCTTTTGGTGA	1260
Query	1261	CTTTATGGAGCCCAAGTTTGAGTTTGCTGTGAAGTTCAATGCACTGGAATTAGATGACAG	1320
Sbjct	1261	 CTTTATGGAGCCCAAGTTTGAGTTTGCTGTGAAGTTCAATGCACTGGAATTAGATGACAG	1320
Query	1321	CGACTTGGCAATATTTATTGCTGTCATTATTCTCAGTGGAGACCGCCCAGGTTTGCTGAA	1380
Sbjct	1321	 CGACTTGGCAATATTTATTGCTGTCATTATTCTCAGTGGAGACCGCCCAGGTTTGCTGAA	1380
Query	1381	TGTGAAGCCCATTGAAGACATTCAAGACAACCTGCTACAAGCCCTGGAGCTCCAGCTGAA	1440

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Sbjct  1381  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 1440
          TGTGAAGCCCATTGAAGACATTCAAGACAACCTGCTACAAGCCCTGGAGCTCCAGCTGAA
Query  1441  GCTGAACCACCCTGAGTCCTCACAGCTGTTTGCCAAGCTGCTCCAGAAAATGACAGACCT 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1441  GCTGAACCACCCTGAGTCCTCACAGCTGTTTGCCAAGCTGCTCCAGAAAATGACAGACCT 1500
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Query  1501  CAGACAGATTGTTCACGGAACACGTGCAGCTACTGCAGGTGATCAAGAAGACGGAGACAGA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1501  CAGACAGATTGTTCACGGAACACGTGCAGCTACTGCAGGTGATCAAGAAGACGGAGACAGA 1560
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Query  1561  CATGAGTCTTCACCCGCTCCTGCAGGAGATCTACAAGGACTTGTACTAG 1609
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1561  CATGAGTCTTCACCCGCTCCTGCAGGAGATCTACAAGGACTTGTACTAG 1609
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